GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: October 26, 2002, 21:04:48 ; Search time 31 Seconds
(without alignments)
827.679 Million cell updates/sec

Title: US-09-840-795-19
Perfect score: 1273
Sequence: 1 MDCQENEYWDQWGRCVTCQR.....AQLFSLDSVPIPQQQQGPEM 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1273	100.0	231	21	AAY77468	Human Rank-like pr
2	1219	95.8	231	22	AAB35335	Human TR14 protein
3	1135	89.2	297	22	AAU03113	Human uterine myom
4	1132	88.9	269	22	AAU03106	Human uterine myom
5	1132	88.9	297	22	AAB29534	Human TNFR homolog
6	1124	88.3	299	22	AAU03116	Composite protein
7	1121	88.1	299	21	AAB30547	Amino acid sequenc
8	1121	88.1	299	21	AAB33477	Human PRO5727 prot
9	1121	88.1	299	22	AAB29533	Human TNFR homolog
10	979	76.9	206	21	AAB01420	Human TANGO 140-1.
11	951	74.7	267	22	AAU03114	Human uterine myom
12	887	69.7	226	22	AAB35330	Human TR14 recepto
13	815	64.0	197	21	AAB01421	Human TANGO 140-2.
14	813	63.9	173	22	AAU03118	Composite protein
15	536	42.1	159	22	AAB35332	Human TNFR related
16	485	38.1	423	20	AAW93581	Human hAPO4-alpha
17	485	38.1	423	21	AAB23547	Human Troy protein
18	483	37.9	328	20	AAY06400	Human NTR-5 recept
19	483	37.9	417	20	AAW98146	Human TRAIN-R. Ho
20	483	37.9	417	21	AAB33474	Human PRO4333 prot
21	483	37.9	417	22	AAU29260	Human PRO polypept
22	483	37.9	417	22	AAU04492	Human TRADE-alpha
23	483	37.9	417	22	AAB82412	Human tumour necro
24	480	37.7	417	19	AAW70386	Amino acid sequenc
25	480	37.7	423	19	AAW70387	Amino acid sequenc
26	480	37.7	423	20	AAW85724	Novel protein (Clo
27	480	37.7	423	22	AAU04493	Human TRADE-beta p
28	478	37.5	416	20	AAW93579	Mouse mAPO4-alpha
29	478	37.5	416	21	AAB23546	Murine Troy protei
30	478	37.5	416	22	AAU04494	Murine TRADE polyp
31	474	37.2	214	20	AAY06522	Mouse STRIFE1 (Tan
32	474	37.2	214	20	AAW98145	Mouse TRAIN-R (lon
33	474	37.2	214	20	AAW93580	Mouse mAPO4-alpha
34	474	37.2	214	21	AAB23548	Murine dTroy prote
35	453	35.6	175	22	AAU03115	Fragment of human
36	443	34.8	77	21	AAY77467	Human Rank-like pr
37	443	34.8	210	20	AAY22223	Human TNFR superfa
38	443	34.8	210	21	AAB28555	Human TNFR soluble
39	410	32.2	150	20	AAW98148	TRAIN-R short, sol
40	406	31.9	150	20	AAY06523	Mouse STRIFE2 (Tan
41	406	31.9	150	20	AAY22224	Mouse TNFR superfa
42	406	31.9	150	20	AAW98144	Mouse TRAIN-R (sho
43	406	31.9	150	20	AAW93583	Mouse mAPO4-gamma
44	406	31.9	150	21	AAB28556	Mouse TNFR soluble
45	406	31.9	150	21	AAY77465	Murine Rank-like p

ALIGNMENTS

RESULT 1
AAY77468
ID AAY77468 standard; Protein; 231 AA.
XX
AC AAY77468;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human Rank-like protein RANKL, SEQ ID NO:23.
XX
KW TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;
KW Rank-like protein; RANKL; immune disorder; inflammation; allergy;
KW immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
KW dermatological; antithyroid.
XX
OS Homo sapiens.
XX
PN WO200001817-A2.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-US12366.
XX
PR 06-JUL-1998; 98US-0110938.
PR 13-JUL-1998; 98US-0114466.
PR 23-JUL-1998; 98US-0093897.
PR 12-AUG-1998; 98US-0132968.
PR 18-AUG-1998; 98US-0136214.
PR 11-SEP-1998; 98US-0099999.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
PI Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;

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PI   Bazan JF,  Mahony D,  Lees EM;
XX
DR   WPI; 2000-171015/15.
DR   N-PSDB; AAZ92411.
XX
PT   New isolated mammalian genes, used to develop products for treating
PT   e.g. immune, inflammatory or allergic abnormalities, cancers or
PT   degenerative conditions -
XX
PS   Claim 24; Page 177-178; 218pp; English.
XX
CC   The invention relates to a number of primate and/or rodent proteins, and
CC   the genes which encode them. The invention encompasses human dendritic
CC   cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis
CC   factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL;
CC   human CC chemokine HCC5; human deubiquitinating proteins Dub11 and Dub
CC   12; human MD-1 and human and murine MD-2 proteins, which exhibit the
CC   properties of ligands for proteins comprising a leucine-rich motif
CC   (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies
CC   against these proteins. The proteins can be used for modulating the
CC   physiology or development of a cell. They can be used to mediate uptake
CC   of substrates (e.g., prostaglandin-like molecules), to modulate or
CC   mediate cellular interactions (e.g., induce or prevent trafficking,
CC   proliferation, or differentiation of cells), or are intracellular
CC   proteins which are important in various cellular processes such as the
CC   deubiquitination of proteins or cell cycle regulation. The products can
CC   be used for treating medical conditions such as immune, inflammatory or
CC   allergic disorders, or abnormal cellular proliferation, for example,
CC   cancers or degenerative conditions. They can be used to modulate immune
CC   responses in disease states e.g., autoimmune disorders, including
CC   rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
CC   autoimmune thyroiditis, as.well as acute and chronic inflammatory
CC   responses in which T cell activation, expansion, and/or immunological T
CC   cell memory play an important role. Sequences AAY77458-Y77461 and
CC   AAY77465-Y77468 represent TNF receptor family-related proteins. AAY77458
CC   is the human protein HDTEA84, AAY77459-Y77461 are human HSLJD37R
CC   proteins, AAY77465 is murine Rank-like protein RANKL, and AAY77466-Y77468
CC   are human RANKL proteins.
XX
SQ   Sequence   231 AA;

  Query Match             100.0%;  Score 1273;  DB 21;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-114;
  Matches  231;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
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Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180

Qy     181 DKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 231
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 231


RESULT 2
AAB35335
ID   AAB35335 standard; Protein; 231 AA.
XX
AC   AAB35335;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TR14 protein SEQ ID NO: 61.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;   99US-0144087.
PR   18-AUG-1999;   99US-0149450.
PR   20-AUG-1999;   99US-0149712.
PR   10-SEP-1999;   99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Young PE;
XX
DR   WPI; 2001-112682/12.
DR   N-PSDB; AAF28049.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 41; Page 413-414; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   231 AA;

  Query Match             95.8%;  Score 1219;  DB 22;  Length 231;
  Best Local Similarity   96.5%;  Pred. No. 2.4e-109;
  Matches  223;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           |||||||||||||||||||||||||||||||||||||||  : |  :||||||||||||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYWHSLPSSQYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTPTSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180

Qy     181 DKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 231
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 231


RESULT 3
AAU03113
ID   AAU03113 standard; Protein; 297 AA.
XX
AC   AAU03113;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human uterine myometrium leiomyoma receptor (UMLR) variant #1.
XX
KW   Human; uterine myometrium leiomyoma receptor; UMLR; ztnfrl1;
KW   tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW   breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
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KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200130850-A1.
XX
PD   03-MAY-2001.
XX
PF   23-OCT-2000; 2000WO-US29304.
XX
PR   22-OCT-1999;   99US-0160880.
PR   02-NOV-1999;   99US-0163215.
PR   17-JUL-2000; 2000US-0218769.
PR   01-AUG-2000; 2000US-0222221.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W,  Lofton-Day CE,  Henne R,  Presnell SR,  Yao Y,  Novak JE;
PI   Foster DC,  Yee DP;
XX
DR   WPI; 2001-300488/31.
XX
PT   Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT   for modulating inflammation, tumour growth, metastasis, cellular
PT   maturation, detecting modulators and as diagnostic indicators of cancer
PT   -
XX
PS   Claim 10; Page 131-132; 148pp; English.
XX
CC   The present sequence represents human uterine myometrium leiomyoma
CC   receptor (UMLR) variant #1. UMLR is a novel member of the tumour
CC   necrosis factor receptor (TNFR) family. The UMLR (also known as ztnfr11)
CC   gene maps to chromosome Xq11-q12. Amino acid residues of UMLR involved in
CC   ligand binding, consisting of residues 1-X (where X is 129-136) are
CC   useful for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC   osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC   or its fragments are useful diagnostically or therapeutically for
CC   identifying tumour cells in uterus melanoma and lung cancer, for
CC   promoting wound healing, and for generating vaccines for cancer therapy.
CC   They are also useful for studying cell-cell interactions, apoptosis,
CC   fertilisation, development, immune recognition, growth control, tumour
CC   suppression and embryo maturation in vitro and in vivo, and for treating
CC   disorders associated with them. UMLR is also useful for identifying
CC   inhibitors of its activity, and for preparing antibodies which can be
CC   used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC   as probes or primers as diagnostic indicators of cancer and for gene
CC   therapy.
XX
SQ   Sequence   297 AA;

  Query Match             89.2%;  Score 1135;  DB 22;  Length 297;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-101;
  Matches  205;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180

Qy     181 DKTAKEESLFPVPPSKETSAESQVS 205
           |||||||||||||||||||||||||
Db     181 DKTAKEESLFPVPPSKETSAESQVS 205


RESULT 4
AAU03106
ID   AAU03106 standard; Protein; 269 AA.
XX
AC   AAU03106;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human uterine myometrium leiomyoma receptor (UMLR).
XX
KW   Human; uterine myometrium leiomyoma receptor; UMLR; ztnfr11;
KW   tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW   breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200130850-A1.
XX
PD   03-MAY-2001.
XX
PF   23-OCT-2000; 2000WO-US29304.
XX
PR   22-OCT-1999;   99US-0160880.
PR   02-NOV-1999;   99US-0163215.
PR   17-JUL-2000; 2000US-0218769.
PR   01-AUG-2000; 2000US-0222221.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W,  Lofton-Day CE,  Henne R,  Presnell SR,  Yao Y,  Novak JE;
PI   Foster DC,  Yee DP;
XX
DR   WPI; 2001-300488/31.
DR   N-PSDB; AAS05944.
XX
PT   Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT   for modulating inflammation, tumour growth, metastasis, cellular
PT   maturation, detecting modulators and as diagnostic indicators of cancer
PT   -
XX
PS   Claim 10; Page 116-117; 148pp; English.
XX
CC   The present sequence representing a novel human uterine myometrium
CC   leiomyoma receptor (UMLR) is a member of the tumour necrosis factor
CC   receptor (TNFR) family. The UMLR (also known as ztnfr11) gene maps to
CC   chromosome Xq11-q12. Amino acid residues of UMLR involved in ligand
CC   binding, consisting of residues 1-X (where X is 129-136) are useful
CC   for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC   osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC   or its fragments are useful diagnostically or therapeutically for
CC   identifying tumour cells in uterus melanoma and lung cancer, for
CC   promoting wound healing, and for generating vaccines for cancer therapy.
CC   They are also useful for studying cell-cell interactions, apoptosis,
CC   fertilisation, development, immune recognition, growth control, tumour
CC   suppression and embryo maturation in vitro and in vivo, and for treating
CC   disorders associated with them. UMLR is also useful for identifying
CC   inhibitors of its activity, and for preparing antibodies which can be
CC   used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC   as probes or primers as diagnostic indicators of cancer and for gene
CC   therapy.
XX
SQ   Sequence   269 AA;

  Query Match             88.9%;  Score 1132;  DB 22;  Length 269;
  Best Local Similarity   97.6%;  Pred. No. 6.8e-101;
  Matches  205;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
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Qy    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180

Qy    181 DKTAKEESLFPVPPSKETSAESQVSWAPGS 210
          |||||||||||||||||||||| |:   |
Db    181 DKTAKEESLFPVPPSKETSAESQESFTMAS 210
```

RESULT 5
AAB29534
ID AAB29534 standard; Protein; 297 AA.
XX
AC AAB29534;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human TNFR homologue, DNA101848.
XX
KW Human; TNFR homologue; tumour necrosis factor receptor; DNA101848;
KW apoptosis; NF-kappa-B activation; proinflammatory response;
KW autoimmune response; modulation; antibody; EDA-A2 inhibition;
KW gene mapping; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200061757-A1.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US09699.
XX
PR 12-APR-1999; 99US-0128849.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J, Yan M;
XX
DR WPI; 2001-070561/08.
DR N-PSDB; AAC63993, AAC63994.
XX
PT New isolated nucleic acid encoding a tumor necrosis factor homolog for
PT modulating apoptosis, NF-kappaB activation, pro-inflammatory or
PT autoimmune response in mammalian cells -
XX
PS Claim 26; Fig 4; 82pp; English.
XX
CC The invention relates to the human tumour necrosis factor receptor
CC (TNFR) homologues DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
CC encoding them (AAC63991, AAC63993), and to the complements (AAC63992,
CC AAC63994) of nucleic acids encoding the TNFR homologues. The invention
CC also relates to vectors and host cells comprising DNA98853 or DNA101848
CC nucleic acids, fusion proteins comprising the DNA98853 or DNA101848
CC proteins, antibodies against the DNA98853 or DNA101848 proteins,
CC recombinant expression of the DNA98853 or DNA101848 proteins. The
CC invention further encompasses a method of modulating apoptosis,
CC NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
CC autoimmune response using the DNA98853 or DNA101848 proteins, and a
CC method of inhibiting or neutralising EDA-A2 protein biological activity
CC in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
CC DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
CC NF-kappa-B activation, proinflammatory or autoimmune responses in
CC mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
CC antibodies) can be used to inhibit or neutralise EDA-A2 protein
CC biological activity in mammalian cells. DNA98853 and DNA101848
CC nucleic acids can be used as hybridisation probes in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, and in gene
CC therapy. The present sequence represents the DNA101848 protein.
XX
SQ Sequence 297 AA;

  Query Match 88.9%; Score 1132; DB 22; Length 297;
  Best Local Similarity 99.5%; Pred. No. 7.7e-101;
  Matches 204; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQS 60

Qy     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180

Qy    181 DKTAKEESLFPVPPSKETSAESQVS 205
          |||||||||||||||||||||||||
Db    181 DKTAKEESLFPVPPSKETSAESQVS 205
```

RESULT 6
AAU03116
ID AAU03116 standard; Protein; 299 AA.
XX
AC AAU03116;
XX
DT 07-SEP-2001 (first entry)
XX
DE Composite protein of human UMLR natural variant #1 with wild type UMLR.
XX
KW Human; uterine myometrium leiomyoma receptor; UMLR; ztnfr11;
KW tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 173..174
FT   /note= "Insertion of Val-Ala compared to wild type
FT   UMLR (AAU03106)"
FT Misc-difference 206..233
FT   /note= "Insertion of 28 amino acid residues
FT   compared to wild type UMLR"
XX
PN WO200130850-A1.
XX
PD 03-MAY-2001.
XX
PF 23-OCT-2000; 2000WO-US29304.
XX
PR 22-OCT-1999; 99US-0160880.
PR 02-NOV-1999; 99US-0163215.
PR 17-JUL-2000; 2000US-0218769.
PR 01-AUG-2000; 2000US-0222221.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Xu W, Lofton-Day CE, Henne R, Presnell SR, Yao Y, Novak JE;
PI Foster DC, Yee DP;
XX
DR WPI; 2001-300488/31.
XX
PT Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT for modulating inflammation, tumour growth, metastasis, cellular
PT maturation, detecting modulators and as diagnostic indicators of cancer
PT -
XX
PS Claim 10; Page 137-138; 148pp; English.
XX
CC The present sequence represents a composite protein of human UMLR
CC natural variant #1 with wild type UMLR (uterine myometrium
CC leiomyoma receptor). UMLR is a novel member of the tumour necrosis

```
CC   factor receptor (TNFR) family. The UMLR (also known as ztnfr11)
CC   gene maps to chromosome Xq11-q12. Amino acid residues of UMLR involved in
CC   ligand binding, consisting of residues 1-X (where X is 129-136) are
CC   useful for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC   osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC   or its fragments are useful diagnostically or therapeutically for
CC   identifying tumour cells in uterus melanoma and lung cancer, for
CC   promoting wound healing, and for generating vaccines for cancer therapy.
CC   They are also useful for studying cell-cell interactions, apoptosis,
CC   fertilisation, development, immune recognition, growth control, tumour
CC   suppression and embryo maturation in vitro and in vivo, and for treating
CC   disorders associated with them. UMLR is also useful for identifying
CC   inhibitors of its activity, and for preparing antibodies which can be
CC   used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC   as probes or primers as diagnostic indicators of cancer and for gene
CC   therapy.
XX
SQ   Sequence   299 AA;

  Query Match            88.3%;  Score 1124;  DB 22;  Length 299;
  Best Local Similarity  99.0%;  Pred. No. 4.6e-100;
  Matches  205;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQR--GGLLQF 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRVAGGLLQF 180

Qy    179 EADKTAKEESLFPVPPSKETSAESQVS 205
          |||||||||||||||||||||||||||
Db    181 EADKTAKEESLFPVPPSKETSAESQVS 207


RESULT 7
AAB30547
ID   AAB30547 standard; Protein; 299 AA.
XX
AC   AAB30547;
XX
DT   06-MAR-2001  (first entry)
XX
DE   Amino acid sequence of a human DNA98853 polypeptide.
XX
KW   Human; DNA58893; full length inverse polymerase chain reaction; FLIP;
KW   inverse long distance PCR.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   74..77
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   24..29
FT                   /note= "potential N-myrsitoylation site"
FT   Modified-site   123..126
FT                   /note= "potential casein kinase II phosphorylati"
FT   Domain          137..158
FT                   /note= "potential transmembrane domain"
FT   Modified-site   185..188
FT                   /note= "potential casein kinase II phosphorylati"
FT   Modified-site   200..203
FT                   /note= "potential casein kinase II phosphorylati"
FT   Modified-site   252..255
FT                   /note= "potential casein kinase II phosphorylati"
FT   Modified-site   257..260
FT                   /note= "potential casein kinase II phosphorylati"
FT   Modified-site   271..274
FT                   /note= "potential casein kinase II phosphorylati"
FT   Modified-site   283..286
FT                   /note= "potential casein kinase II phosphorylati"
XX
PN   WO200061741-A1.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09554.
XX
PR   12-APR-1999;   99US-0128849.
PR   10-JAN-2000; 2000US-0480782.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Chui CJ,  Grimaldi JC,  Milton S,  Yan M,  Yi S;
XX
DR   WPI; 2000-679484/66.
XX
PT   New polymerase chain based cloning method for isolating a nucleic acid
PT   molecule of interest from a mixture of nucleic acid molecules using
PT   full length inverse PCR -
XX
PS   Example 2; Fig 5; 31pp; English.
XX
CC   The present sequence represents a human DNA98853 polypeptide. The
CC   DNA98853 gene was amplified and cloned using a PCR-based method of
CC   the invention, called full length inverse polymerase chain reaction
CC   (FLIP). FLIP is also referred to as inverse long distance PCR,
CC   because of its ability to isolate long genes. The specification uses
CC   FLIP for amplifying and isolating a nucleic acid molecule of interest
CC   from a mixture of nucleic acid molecules. The method is useful for
CC   efficiently cloning a wide variety of genes.
XX
SQ   Sequence   299 AA;

  Query Match            88.1%;  Score 1121;  DB 21;  Length 299;
  Best Local Similarity  98.6%;  Pred. No. 8.9e-100;
  Matches  204;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db      1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQS 60

Qy     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQR--GGLLQF 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db    121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRVTGGLLQF 180

Qy    179 EADKTAKEESLFPVPPSKETSAESQVS 205
          |||||||||||||||||||||||||||
Db    181 EADKTAKEESLFPVPPSKETSAESQVS 207


RESULT 8
AAB33477
ID   AAB33477 standard; Protein; 299 AA.
XX
AC   AAB33477;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO5727 protein UNQ2448 SEQ ID NO:297.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
```

KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 23-MAR-1999; 99US-0125775.
PR 12-APR-1999; 99US-0128849.
PR 20-APR-1999; 99WO-US08615.
PR 28-APR-1999; 99US-0131445.
PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58642.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS Claim 33; Fig 128; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 299 AA;

Query Match 88.1%; Score 1121; DB 21; Length 299;
Best Local Similarity 98.6%; Pred. No. 8.9e-100;
Matches 204; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

```
Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQR--GGLLQF 178
           |||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRVTGGLLQF 180

Qy     179 EADKTAKEESLFPVPPSKETSAESQVS 205
           |||||||||||||||||||||||||||
Db     181 EADKTAKEESLFPVPPSKETSAESQVS 207
```

RESULT 9
AAB29533
ID AAB29533 standard; Protein; 299 AA.
XX
AC AAB29533;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human TNFR homologue, DNA98853.
XX
KW Human; TNFR homologue; tumour necrosis factor receptor; DNA98853;
KW apoptosis; NF-kappa-B activation; proinflammatory response;
KW autoimmune response; modulation; antibody; EDA-A2 inhibition;
KW gene mapping; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200061757-A1.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US09699.
XX
PR 12-APR-1999; 99US-0128849.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J, Yan M;
XX
DR WPI; 2001-070561/08.
DR N-PSDB; AAC69331, AAC69332.

```
XX
PT   New isolated nucleic acid encoding a tumor necrosis factor homolog for
PT   modulating apoptosis, NF-kappaB activation, pro-inflammatory or
PT   autoimmune response in mammalian cells -
XX
PS   Claim 1; Fig 2; 82pp; English.
XX
CC   The invention relates to the human tumour necrosis factor receptor
CC   (TNFR) homologues DNA98853 (AAB29533) and DNA101848 (AAB29534), to cDNA
CC   encoding them (AAC63991, AAC63993), and to the complements (AAC63992,
CC   AAC63994) of nucleic acids encoding the TNFR homologues. The invention
CC   also relates to vectors and host cells comprising DNA98853 or DNA101848
CC   nucleic acids, fusion proteins comprising the DNA98853 or DNA101848
CC   proteins, antibodies against the DNA98853 or DNA101848 proteins,
CC   recombinant expression of the DNA98853 or DNA101848 proteins. The
CC   invention further encompasses a method of modulating apoptosis,
CC   NF-kappa-B (nuclear factor kappa-B) activation, or a proinflammatory or
CC   autoimmune response using the DNA98853 or DNA101848 proteins, and a
CC   method of inhibiting or neutralising EDA-A2 protein biological activity
CC   in mammalian cells using DNA98853 or DNA101848-specific antibodies. The
CC   DNA98853 and/or DNA101848 proteins can be used for modulating apoptosis,
CC   NF-kappa-B activation, proinflammatory or autoimmune responses in
CC   mammalian cells. DNA98853 and/or DNA101848 protein immunoadhesins (e.g.,
CC   antibodies) can be used to inhibit or neutralise EDA-A2 protein
CC   biological activity in mammalian cells. DNA98853 and DNA101848
CC   nucleic acids can be used as hybridisation probes in chromosome and gene
CC   mapping, in the generation of antisense RNA and DNA, and in gene
CC   therapy. The present sequence represents the DNA98853 protein.
XX
SQ   Sequence   299 AA;

  Query Match             88.1%;  Score 1121;  DB 22;  Length 299;
  Best Local Similarity   98.6%;  Pred. No. 8.9e-100;
  Matches  204;  Conservative    1;  Mismatches    0;  Indels    2;  Gaps    1;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||| |
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHRCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQR--GGLLQF 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRVTGGLLQF 180

Qy     179 EADKTAKEESLFPVPPSKETSAESQVS 205
           |||||||||||||||||||||||||||
Db     181 EADKTAKEESLFPVPPSKETSAESQVS 207


RESULT 10
AAB01420
ID   AAB01420 standard; Protein; 206 AA.
XX
AC   AAB01420;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Human TANGO 140-1.
XX
KW   TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW   graft versus-host diseases; rheumatoid arthritis; psoriasis;
KW   inflammatory bowel disease; septic shock; ulcerative colitis;
KW   Crohn's disease; chronic myelogenous leukemia; cancer; liver
KW   disease; Hodgkin's disease; osteoarthritis; Lyme's disease;
KW   cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes;
KW   systemic lupus erythematosus; transgenic animal; diagnosis;
KW   prognosis; prophylatic; therapeutic; human.
XX
OS   Homo sapiens.
XX
PN   WO200039284-A1.
XX
PD   06-JUL-2000.
XX
PF   23-DEC-1999;   99WO-US31025.
XX
PR   30-DEC-1998;   98US-0223546.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Holtzman DA;
XX
DR   WPI; 2000-465743/40.
DR   N-PSDB; AAA47453.
XX
PT   Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,
PT   224 and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT   arthritis, psoriasis and autoimmune diseases
XX
PS   Claim 8; Fig 2; 209pp; English.
XX
CC   Nucleic acids encoding TANGO polypeptides are useful as modulating
CC   agents for regulating cellular processes like asthma, graft
CC   versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory
CC   bowel disease, septic shock, ulcerative colitis, Crohn's disease,
CC   chronic myelogenous leukemia, cancer, liver disease, Hodgkin's
CC   disease, osteoarthritis, Lyme's disease, cachexia and autoimmune
CC   diseases e.g. myasthemia gravis, autoimmune diabetes and systemic
CC   lupus erythematosus. The nucleic acids are also useful for producing
CC   transgenic animals and the TANGO polypeptides themselves. Partial
CC   TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in
CC   forensic biology, for diagnostic assays, prognostic assays,
CC   pharmacogenomics and for monitoring clinical trials. TANGO
CC   polypeptides are suitable for both prophylactic and therapeutic
CC   methods for treating a subject at risk of a disorder or having a
CC   disorder associated with aberrant TANGO expression. A wide range
CC   of cellular disorders can be treated.
XX
SQ   Sequence   206 AA;

  Query Match             76.9%;  Score 979;  DB 21;  Length 206;
  Best Local Similarity   95.1%;  Pred. No. 2.7e-86;
  Matches  175;  Conservative    2;  Mismatches    5;  Indels    2;  Gaps    1;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 68

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 128

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQR--GGLLQF 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||    |
Db     129 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGKGGCFMF 188

Qy     179 EADK 182
             ::
Db     189 HMNQ 192


RESULT 11
AAU03114
ID   AAU03114 standard; Protein; 267 AA.
XX
AC   AAU03114;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human uterine myometrium leiomyoma receptor (UMLR) variant #2.
XX
KW   Human; uterine myometrium leiomyoma receptor; UMLR; ztnfr11;
KW   tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
```

```
KW   breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200130850-A1.
XX
PD   03-MAY-2001.
XX
PF   23-OCT-2000; 2000WO-US29304.
XX
PR   22-OCT-1999;   99US-0160880.
PR   02-NOV-1999;   99US-0163215.
PR   17-JUL-2000; 2000US-0218769.
PR   01-AUG-2000; 2000US-0222221.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W,  Lofton-Day CE,  Henne R,  Presnell SR,  Yao Y,  Novak JE;
PI   Foster DC,  Yee DP;
XX
DR   WPI; 2001-300488/31.
XX
PT   Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT   for modulating inflammation, tumour growth, metastasis, cellular
PT   maturation, detecting modulators and as diagnostic indicators of cancer
PT   -
XX
PS   Claim 10; Page 133-134; 148pp; English.
XX
CC   The present sequence represents human uterine myometrium leiomyoma
CC   receptor (UMLR) variant #2. UMLR is a novel member of the tumour
CC   necrosis factor receptor (TNFR) family. The UMLR (also known as ztnfr11)
CC   gene maps to chromosome Xq11-q12. Amino acid residues of UMLR involved in
CC   ligand binding, consisting of residues 1-X (where X is 129-136) are
CC   useful for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC   osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC   or its fragments are useful diagnostically or therapeutically for
CC   identifying tumour cells in uterus melanoma and lung cancer, for
CC   promoting wound healing, and for generating vaccines for cancer therapy.
CC   They are also useful for studying cell-cell interactions, apoptosis,
CC   fertilisation, development, immune recognition, growth control, tumour
CC   suppression and embryo maturation in vitro and in vivo, and for treating
CC   disorders associated with them. UMLR is also useful for identifying
CC   inhibitors of its activity, and for preparing antibodies which can be
CC   used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC   as probes or primers as diagnostic indicators of cancer and for gene
CC   therapy.
XX
SQ   Sequence   267 AA;

  Query Match             74.7%;  Score 951;  DB 22;  Length 267;
  Best Local Similarity   85.4%;  Pred. No. 1.8e-83;
  Matches  175;  Conservative    0;  Mismatches    0;  Indels   30;  Gaps    1;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120

Qy     121 QLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQFEA 180
           ||||||||||||||||||||                              ||||||||
Db     121 QLSLVEADAPTVPPQEATLVAL------------------------------GGLLQFEA 150

Qy     181 DKTAKEESLFPVPPSKETSAESQVS 205
           |||||||||||||||||||||||||
Db     151 DKTAKEESLFPVPPSKETSAESQVS 175


RESULT 12
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AAB35330
ID   AAB35330 standard; Protein; 226 AA.
XX
AC   AAB35330;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TR14 receptor protein SEQ ID NO: 5.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;   99US-0144087.
PR   18-AUG-1999;   99US-0149450.
PR   20-AUG-1999;   99US-0149712.
PR   10-SEP-1999;   99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Young PE;
XX
DR   WPI; 2001-112682/12.
DR   N-PSDB; AAF27998.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 24; Page 376; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   226 AA;

  Query Match             69.7%;  Score 887;  DB 22;  Length 226;
  Best Local Similarity   97.1%;  Pred. No. 2.2e-77;
  Matches  169;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      58 CQSCITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQ 117
           |:   ||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      53 CRVACTCAVINRVQKVNCTPTSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQ 112

Qy     118 CAFQLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQ 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     113 CAFQLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQFFNRHCQRGGLLQ 172

Qy     178 FEADKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 231
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 FEADKTAKEESLFPVPPSKETSAESQVSWAPGSLAQLFSLDSVPIPQQQQGPEM 226


RESULT 13
AAB01421
ID   AAB01421 standard; Protein; 197 AA.
XX
AC   AAB01421;
XX
DT   20-OCT-2000  (first entry)
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XX
DE   Human TANGO 140-2.
XX
KW   TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW   graft versus-host diseases; rheumatoid arthritis; psoriasis;
KW   inflammatory bowel disease; septic shock; ulcerative colitis;
KW   Crohn's disease; chronic myelogenous leukemia; cancer; liver
KW   disease; Hodgkin's disease; osteoarthritis; Lyme's disease;
KW   cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes;
KW   systemic lupus erythematosus; transgenic animal; diagnosis;
KW   prognosis; prophylatic; therapeutic; human.
XX
OS   Homo sapiens.
XX
PN   WO200039284-A1.
XX
PD   06-JUL-2000.
XX
PF   23-DEC-1999;   99WO-US31025.
XX
PR   30-DEC-1998;   98US-0223546.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Holtzman DA;
XX
DR   WPI; 2000-465743/40.
DR   N-PSDB; AAA47454.
XX
PT   Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,
PT   224 and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT   arthritis, psoriasis and autoimmune diseases
XX
PS   Claim 8; Fig 3; 209pp; English.
XX
CC   Nucleic acids encoding TANGO polypeptides are useful as modulating
CC   agents for regulating cellular processes like asthma, graft
CC   versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory
CC   bowel disease, septic shock, ulcerative colitis, Crohn's disease,
CC   chronic myelogenous leukemia, cancer, liver disease, Hodgkin's
CC   disease, osteoarthritis, Lyme's disease, cachexia and autoimmune
CC   diseases e.g. myasthemia gravis, autoimmune diabetes and systemic
CC   lupus erythematosus. The nucleic acids are also useful for producing
CC   transgenic animals and the TANGO polypeptides themselves. Partial
CC   TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in
CC   forensic biology, for diagnostic assays, prognostic assays,
CC   pharmacogenomics and for monitoring clinical trials. TANGO
CC   polypeptides are suitable for both prophylactic and therapeutic
CC   methods for treating a subject at risk of a disorder or having a
CC   disorder associated with aberrant TANGO expression. A wide range
CC   of cellular disorders can be treated.
XX
SQ   Sequence   197 AA;

  Query Match             64.0%;  Score 815;  DB 21;  Length 197;
  Best Local Similarity   97.3%;  Pred. No. 1.6e-70;
  Matches  142;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 82

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      83 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 142

Qy     121 QLSLVEADAPTVPPQEATLVALVSSL 146
           |||||||||||||||||||||:  :
Db     143 QLSLVEADAPTVPPQEATLVALLQEV 168


RESULT 14
AAU03118
ID   AAU03118 standard; Protein; 173 AA.
XX
AC   AAU03118;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Composite protein of human UMLR natural variant #2 with wild type UMLR.
XX
KW   Human; uterine myometrium leiomyoma receptor; UMLR; ztnfr11;
KW   tumour necrosis factor receptor; TNFR; chromosome Xq11-q12; lung cancer;
KW   breast carcinoma; uterus melanoma; osteosarcoma; lymphoma; wound healing;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200130850-A1.
XX
PD   03-MAY-2001.
XX
PF   23-OCT-2000; 2000WO-US29304.
XX
PR   22-OCT-1999;   99US-0160880.
PR   02-NOV-1999;   99US-0163215.
PR   17-JUL-2000; 2000US-0218769.
PR   01-AUG-2000; 2000US-0222221.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Xu W,  Lofton-Day CE,  Henne R,  Presnell SR,  Yao Y,  Novak JE;
PI   Foster DC,  Yee DP;
XX
DR   WPI; 2001-300488/31.
XX
PT   Uterine myometrium leiomyoma receptor polypeptides and polynucleotides
PT   for modulating inflammation, tumour growth, metastasis, cellular
PT   maturation, detecting modulators and as diagnostic indicators of cancer
PT   -
XX
PS   Claim 2; Page 139; 148pp; English.
XX
CC   The present sequence represents a composite protein of human UMLR
CC   natural variant #2 with wild type UMLR (uterine myometrium
CC   leiomyoma receptor). UMLR is a novel member of the tumour necrosis
CC   factor receptor (TNFR) family. The UMLR (also known as ztnfr11)
CC   gene maps to chromosome Xq11-q12. Amino acid residues of UMLR involved in
CC   ligand binding, consisting of residues 1-X (where X is 129-136) are
CC   useful for inhibiting the quantity of lung, breast carcinoma, melanoma,
CC   osteosarcoma or lymphoma cells expressing UMLR protein. UMLR polypeptides
CC   or its fragments are useful diagnostically or therapeutically for
CC   identifying tumour cells in uterus melanoma and lung cancer, for
CC   promoting wound healing, and for generating vaccines for cancer therapy.
CC   They are also useful for studying cell-cell interactions, apoptosis,
CC   fertilisation, development, immune recognition, growth control, tumour
CC   suppression and embryo maturation in vitro and in vivo, and for treating
CC   disorders associated with them. UMLR is also useful for identifying
CC   inhibitors of its activity, and for preparing antibodies which can be
CC   used to detect UMLR expression. UMLR polynucleotide sequences are useful
CC   as probes or primers as diagnostic indicators of cancer and for gene
CC   therapy.
XX
SQ   Sequence   173 AA;

  Query Match             63.9%;  Score 813;  DB 22;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-70;
  Matches  142;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQS 60

Qy      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAF 120
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Qy    121 QLSLVEADAPTVPPQEATLVAL 142
          |||||||||||||||||||||||
Db    121 QLSLVEADAPTVPPQEATLVAL 142


RESULT 15
AAB35332
ID   AAB35332 standard; Protein; 159 AA.
XX
AC   AAB35332;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TNFR related protein SEQ ID NO: 7.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;   99US-0144087.
PR   18-AUG-1999;   99US-0149450.
PR   20-AUG-1999;   99US-0149712.
PR   10-SEP-1999;   99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Young PE;
XX
DR   WPI; 2001-112682/12.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Disclosure; Page 378; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   159 AA;

  Query Match             42.1%;  Score 536;  DB 22;  Length 159;
  Best Local Similarity   95.3%;  Pred. No. 9e-44;
  Matches  102;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     58 CQSCITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQ 117
          |:   ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     53 CRVACTCAVINRVQKVNCTPTSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQ 112

Qy    118 CAFQLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQ 164
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 CAFQLSLVEADAPTVPPQEATLVALVSSLLVVFTLAFLGLFFLYCKQ 159


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Job time : 32 secs
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